537736.trn

08/537,736

SRNT

```
=> search combination or combinator?
        167630 COMBINATION
           988 COMBINATOR?
L1      168549 COMBINATION OR COMBINATOR?

=> s l1(2a)chemistry
        337636 CHEMISTRY
L2          29 L1(2A)CHEMISTRY

=> d bib

L2   ANSWER 1 OF 29  MEDLINE
AN   96368010     MEDLINE
TI   Characterization of the complexity of small-molecule libraries of
     electrospray ionization mass spectrometry.
AU   Dunayevskiy Y; Vouros P; Carell T; Wintner E A; Rebek J Jr
CS   Department of Chemistry, Barnett Institute, Northeastern University,
     Boston, Massachusetts 02115, USA.
SO   ANALYTICAL CHEMISTRY, (1995 Sep 1) 67 (17) 2906-15.
     Journal code: 4NR. ISSN: 0003-2700.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
EM   9611

=> d all

L2   ANSWER 1 OF 29  MEDLINE
AN   96368010     MEDLINE
TI   Characterization of the complexity of small-molecule libraries of
     electrospray ionization mass spectrometry.
AU   Dunayevskiy Y; Vouros P; Carell T; Wintner E A; Rebek J Jr
CS   Department of Chemistry, Barnett Institute, Northeastern University,
     Boston, Massachusetts 02115, USA.
SO   ANALYTICAL CHEMISTRY, (1995 Sep 1) 67 (17) 2906-15.
     Journal code: 4NR. ISSN: 0003-2700.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
EM   9611
AB   The growing interest in   ***combinatorial***     ***chemistry***
     has led us to explore new analytical methods for the analysis of
     complex molecular libraries. Because an investigation of large
     mixtures with 10(4)-10(5) different chemical entities was not
     realistic, an alternative approach was pursued that included the
     analysis of small representative sublibraries using positive and
     negative ion electrospray mass spectrometry. The detailed analysis
     of these model mixtures, containing up to 55 components, allowed us
     to obtain important information about the composition of a library
     with considerable complexity. The results were used to improve the
     synthetic procedure in order to provide the maximum yield of
     expected library components. The applicability of mass spectrometry
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      to the analysis of complex matrices and the usefulness of the
      technique for screening synthesized combinatorial libraries to probe
      their expected diversity and complexity have been demonstrated.
CT     Amino Acid Sequence
      *Dipeptides: CH, chemistry
       Molecular Sequence Data
       Spectrum Analysis, Mass
CN    0 (Dipeptides)

=> e review/dt
E1          231      RETRACTED PUBLICATION/DT
E2          198      RETRACTION OF PUBLICATION/DT
E3       517153 --> REVIEW/DT
E4        34742      REVIEW ACADEMIC/DT
E5        12627      REVIEW LITERATURE/DT
E6         4854      REVIEW MULTICASE/DT
E7        25959      REVIEW OF REPORTED CASES/DT
E8       268783      REVIEW TUTORIAL/DT
E9           13      SCIENTIFIC INTEGRITY REVIEW/DT
E10         392      TECHNICAL REPORT/DT
E11         250      TWIN STUDY/DT
**** END OF FIELD ****

=> s e3-8
         517153 REVIEW/DT
          34742 "REVIEW ACADEMIC"/DT
          12627 "REVIEW LITERATURE"/DT
           4854 "REVIEW MULTICASE"/DT
          25959 "REVIEW OF REPORTED CASES"/DT
         268783 "REVIEW TUTORIAL"/DT
L3       517189 (REVIEW/DT OR "REVIEW ACADEMIC"/DT OR "REVIEW LITERATURE"/
                DT OR "REVIEW MULTICASE"/DT OR "REVIEW OF REPORTED CASES"/
                DT OR "REVIEW TUTORIAL"/DT)

=> d his

     (FILE 'HOME' ENTERED AT 21:45:29 ON 10 OCT 96)

     FILE 'MEDLINE' ENTERED AT 21:45:32 ON 10 OCT 96
L1        168549 SEARCH COMBINATION OR COMBINATOR?
L2            29 S L1(2A)CHEMISTRY
                  E REVIEW/DT
L3        517189 S E3-8

=> s l3 and l2
L4             5 L3 AND L2

=> d 1-5 all

L4   ANSWER 1 OF 5  MEDLINE
AN   96166348     MEDLINE
TI     ***Combinatorial***      ***chemistry***   in the discovery and
     development of drugs.
```

AU Doyle P M
CS Department of Medic[redacted]l Chemistry, Wellcome Res[redacted]rch Laboratories, Beckenham, Kent, UK.
SO JOURNAL OF CHEMICAL TECHNOLOGY AND BIOTECHNOLOGY, (1995 Dec) 64 (4) 317-24. Ref: 70
Journal code: AL8. ISSN: 0268-2575.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals; B
EM 9605
CT Amino Acid Sequence
Automation
Databases, Factual
*Drug Design
Molecular Sequence Data
Oligopeptides: CH, chemistry
*Oligopeptides: CS, chemical synthesis
CN 0 (Oligopeptides)

L4 ANSWER 2 OF 5 MEDLINE
AN 96102839 MEDLINE
TI Solid-phase ***combinatorial*** ***chemistry*** and novel tagging methods for identifying leads.
AU Chabala J C
CS Phamacopeia Inc, Princeton, USA.
SO CURRENT OPINION IN BIOTECHNOLOGY, (1995 Dec) 6 (6) 632-9. Ref: 24
Journal code: A92. ISSN: 0958-1669.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 9604
AB Encoded combinatorial chemical synthesis on solid phase is a new paradigm in organic chemistry that provides chemists with powers similar to those enjoyed by molecular biologists. Encoded chemical libraries will have a profound impact on all endeavors that seek to identify molecules with optimized properties and to understand the factors governing molecular interactions. In particular, the discovery and optimization of new therapeutic and diagnostic drug molecules, traditionally a slow manual process, will be greatly accelerated by this technology.
CT Amino Acid Sequence
Biotechnology
Chemistry, Organic
Drug Design
Molecular Sequence Data
Oligonucleotides: GE, genetics
Oligopeptides: CH, chemistry

*Oligopeptides: CS, chemical synthesis
Oligopeptides: GE, genetics
CN 0 (Oligonucleotides); 0 (Oligopeptides)

L4 ANSWER 3 OF 5 MEDLINE
AN 96050146 MEDLINE
TI Strategies and recent technologies in drug discovery.
AU Kubinyi H
CS Drug Design, BASF, Ludwigshafen.
SO PHARMAZIE, (1995 Oct) 50 (10) 647-62. Ref: 311
Journal code: P4D. ISSN: 0031-7144.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 9603
AB In the last years, the paradigms of drug research changed significantly. New technologies were developed, in several different fields. ***Combinatorial*** ***chemistry*** and high-throughput screening increase our chances to find new lead structures, with less effort than by dedicated syntheses. Gene technology, in addition to providing therapeutically useful proteins, significantly contributes to rational drug design. The primary structure of a protein can be derived from the DNA sequence of the corresponding gene. Its relevance for a certain disease is investigated in transgenic animals. Expression of the protein in bacteria or in cell culture produces material for screening systems and for 3D structure determination by protein crystallography. NMR techniques, or electron cryo-microscopy. Structure-based and computer-aided design methods are applied to optimize lead structures with the least effort. A serious problem in the application of such techniques is their limitation to ligand-protein interactions. For the design of a therapeutically useful drug, also absorption, distribution, metabolism and elimination have to be considered. QSAR methods help in this respect. Scope and limitations of the new technologies are discussed in the context of conventional approaches in drug discovery.
CT Check Tags: Animal; Human; Support, Non-U.S. Gov't
Genetic Engineering
*Pharmacology: TD, trends
Research Design
Technology, Pharmaceutical

L4 ANSWER 4 OF 5 MEDLINE
AN 94176088 MEDLINE
TI ***Combinatorial*** ***chemistry*** --applications of light-directed chemical synthesis.
AU Jacobs J W; Fodor S P
CS Affymax Research Institute, Palo Alto, CA 94304..
SO TRENDS IN BIOTECHNOLOGY, (1994 Jan) 12 (1) 19-26. Ref: 29
Journal code: ALJ. ISSN: 0167-7799.

CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS B
EM 9406
AB Combinatorial methods in biology and chemistry are proving to be powerful methods for generating molecular diversity. One approach, light-directed chemical synthesis, combines semiconductor-based photolithography technologies with solid-phase organic chemistry to synthesize large arrays of molecules with potential biological activity. This novel technology has the potential to provide libraries of both natural and synthetic molecules that might be screened rapidly for biological activity.
CT Amino Acid Sequence
Base Sequence
Biotechnology: MT, methods
Carbamates: CH, chemistry
Dynorphins: AA, analogs & derivatives
Dynorphins: CH, chemistry
Dynorphins: CS, chemical synthesis
Dynorphins: GE, genetics
DNA: GE, genetics
Endorphins: CH, chemistry
Endorphins: CS, chemical synthesis
Endorphins: GE, genetics
Molecular Sequence Data
Oligonucleotides: CH, chemistry
*Oligonucleotides: CS, chemical synthesis
Oligonucleotides: GE, genetics
Peptides: CH, chemistry
*Peptides: CS, chemical synthesis
Peptides: GE, genetics
*Photochemistry: MT, methods
RN 74913-18-1 (Dynorphins); 83335-41-5 (rimorphin); 9007-49-2 (DNA)
CN 0 (Carbamates); 0 (Endorphins); 0 (Oligonucleotides); 0 (Peptides)

L4 ANSWER 5 OF 5 MEDLINE
AN 90058642 MEDLINE
TI Polypeptide chain binding proteins: catalysts of protein folding and related processes in cells.
AU Rothman J E
CS Department of Biology, Princeton University, New Jersey 08544..
SO CELL, (1989 Nov 17) 59 (4) 591-601. Ref: 102
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals; Cancer Journals
EM 9003

AB Subcellular compartments in which folding and assembly of proteins occur seem to have [redacted]set of PCB proteins capabl[redacted]of mediating these and related processes, such as translocation across membranes. When a domain of a polypeptide chain emerges from a ribosome during synthesis or from the distal side of a membrane during translocation, successive segments of the chain are incrementally exposed to solvent and yet are unlikely to be able to fold. This topological restriction on folding likely mandates a need for PCB proteins to prevent aggregation. Catalysis of topologically restricted folding by PCB proteins is likely to involve both an antifolding activity that postpones folding until entire domains are available and, more speculatively, a folding activity resulting from a programmed stepwise release that employs the energy of ATP hydrolysis to ensure a favorable pathway. We are left with a new set of problems. How do proteins fold in cells? What are the sequences or structural signals that dictate folding pathways? The new challenge will be to understand folding as a ***combination*** of physical ***chemistry*** , enzymology, and cell biology.

CT Check Tags: Animal
Antigens, Bacterial: ME, metabolism
*Heat-Shock Proteins: ME, metabolism
*Protein Conformation

CN 0 (Antigens, Bacterial); 0 (GroEL Protein); 0 (Heat-Shock Proteins)

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	2.80	2.95

STN INTERNATIONAL LOGOFF AT 21:49:19 ON 10 OCT 96

L3 ANSWER 1 OF 1 SCISEARCH COPYRIGHT 1996 ISI (R)
AN 94:118410 SCISEARCH
GA The Genuine Article (R) Number: MV090
TI COMBINATORIAL CHEMISTRY - APPLICATIONS OF LIGHT-DIRECTED CHEMICAL SYNTHESIS
AU JACOBS J W (Reprint); FODOR S P A
CS AFFYMAX RES INST, 4001 MIRANDA AVE, PALO ALTO, CA, 94304 (Reprint); AFFYMETRIX, SANTA CLARA, CA, 95051
CYA USA
SO TRENDS IN BIOTECHNOLOGY, (JAN 1994) Vol. 12, No. 1, pp. 19-26. ISSN: 0167-9430.
DT General Review; Journal
FS AGRI
LA ENGLISH
REC Reference Count: 29
AB Combinatorial methods in biology and chemistry are proving to be powerful methods for generating molecular diversity. One approach, light-directed chemical synthesis, combines semiconductor-based photolithography technologies with solid-phase organic chemistry to synthesize large arrays of molecules with potential biological activity. This novel technology has the potential to provide libraries of both natural and synthetic molecules that might be screened rapidly for biological activity.
CC BIOTECHNOLOGY & APPLIED MICROBIOLOGY
STP KeyWords Plus (R): DRUG DISCOVERY; LIGANDS; LIBRARY; MOLECULES
RF 92-0799 007; ANTIBODY ENGINEERING; ANTIGEN COMBINING SITE; FILAMENTOUS PHAGE; PROTEIN TARGETS
92-5823 001; B-CELL EPITOPES OF THE CHLAMYDIA-TRACHOMATIS MAJOR OUTER-MEMBRANE PROTEIN; PEPTIDE LIBRARIES; ANTIGENIC SITES; ANTIPEPTIDE ANTIBODIES
RE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)
BARRETT R W	1985	6	113	NEUROPEPTIDES
BIRNBAUM S	1992	3	49	CURR OPIN BIOTECH
BRENNER S	1992	89	5381	P NATL ACAD SCI USA
BUNIN B A	1992	114	10997	J AM CHEM SOC
CARUTHERS M H	1985	230	281	SCIENCE
CHO C Y	1993	261	1303	SCIENCE
CWIRLA S E	1990	87	6378	P NATL ACAD SCI USA
DEVLIN J J	1990	249	404	SCIENCE
DOWER W J	1992	2	251	CURR BIOL
ELLINGTON A D	1990	346	818	NATURE
FODOR S P A	1993	364	555	NATURE
FODOR S P A	1991	251	767	SCIENCE
FRANK R	1992	48	9217	TETRAHEDRON
FURKA A	1991	37	487	INT J PEPT PROT RES
GEYSEN H M	1984	81	3998	P NATL ACAD SCI USA
HOLMES C P	1993		489	PERSPECTIVES MED CHE
HOUGHTEN R A	1991	354	84	NATURE

KERR J M	1993	115	2529	J AM CHEM SOC
LAM K S	1991	354	82	NATURE
MERRIFIELD R B	1963	85	2149	J AM CHEM SOC
MERRIFIELD R B	1986	232	341	SCIENCE
NEEDELS M C	1993	90	10700	P NATL ACAD SCI USA
NIKOLAIEV V	1993	6	161	PEPTIDE RES
PAVIA M R	1993	3	387	BIOORG MED CHEM LETT
PEASE A C				IN PRESS P NATL ACAD
SCOTT J K	1990	249	386	SCIENCE
SIMON R J	1992	89	9367	P NATL ACAD SCI USA
TUERK C	1990	249	505	SCIENCE
WELLS J A	1992	2	597	CURR OPIN STRUC BIOL